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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: pir3:*
4: pir4:*
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c;Species; Streptococcus pneumoniae
c;Date: 03-Aug-2001 *sequence_revision 03-Aug-2001 *text_change 24-Aug-2001
c;Accession: G9522
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtza,
nson, T.; Hickey, E.K.; Holt, I.E.
science 293, 498-506, 2001
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor.
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor.
A;Authors: Ag5000; MUID:21357209; PMID:11463916
A;Accession: G95222
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A;Molecule type: DNA
A;Residues: 1-940 <KUR>
A;Cross references: GB:AB005672; PIDN:AAK75976.1; PID:g14973411; GSPDB:GN00164; TI
A;Dexperimental source: strain TIGR4
C;Genetics:
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EKLQERLAKLAGGVAVIKVGAPTETALKEMKLRIEDALNATRAAVEEGIVAGGGTALITV
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                                                             EDLGLELKDATIEALGQAARVTVDKDSTVIVEGAGNPEAISHRVAVIKSQIETTTSEFDR
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H819596
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C41325
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A26950
A43509
S23918
I40331
AB2043
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authbrs: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H98086
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c;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: H99086
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; De
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Best Local Similarity 87.6
Matches 477; Conservative
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;Molecule type: DNA
;Residues: 1-540 <KUR>
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                                                                              EKLQERLAKLAGGVAVIKVGAPTETALKEMKLRIEDALNATRAAVEEGIVAGGGTALITV
                                                                                                                       IPAVATLELTGDEATGRNIVLRALEEPVRQIAHNAGFEGSIVIDRLKNAELGIGFNAATG
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87.8%; Pred. No. 9.7e-110;
ative 34; Mismatches 28;
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886674
806074
Strain [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
60 KD chaperonin [imported] - Lactococcus lactis
C:Species: Lactococcus lactis subsp. lactis
C:Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A;Residues: 1-542 <STO>
A;Cross-references: GB:AE005176; PID:g12723267; PIDN:AAK04492.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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R;Motorin, A.; Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; El Genome Rss. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lacti: A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: B86674
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Best Local
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;Superfamily: chaperonin
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| MOTELDVVEGMQFDRGYLSQYMVSNTEKMVAELDNPYILITDKKISNIQEILPLLEQILK
                                                        QWVNMIEEGIVDPAKVTRSALQNAASVAGLILTTEAVVANKPEPA - APAMPP-MDPSM-
                                                                          EWVDMIKTGIIDPVKVTRSALQNAASVASLILTTEAVVANKPEPATPAPAMPAGMDPGMM 540
                                                                                                                                          IEKVAALELEGDDATGRNIVLRALEEPVRQIALNAGYEGSVVIDKLKNSPAGTGFNAATG 480
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-GMGG
                                                                                                                     IAALDKLSEEGDIQTGINIVRRALEEPVRQIAANAGYEGSVIIDKLRSEEVGTGFNAATG
                                                                                                                                                                                EKLQERLAKLAGGVAVVKVGAATETELKAMKLLIEDALNATRAAVEEGIVSGGGTALVNA
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540
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3.4e-102;
heg 46;
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groEL protein - Lactococcus lactis
C;Specles: Lactococcus lactis
C;Date: 05-Jan-1995 #sequence_revision
C;Accession: S32106
R;Batt, C.A.
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R;Kim, S.G.; Batt, C.A.
Gene 127, 121-126, 1993
A;Title: Cloning and sequencing of Lactococcus lactis subsp. lactis groESL operon.
A;Reference number: JN0660; MUID:93252268; PMID:8486277
A;Accession: JN0661
A;Molecule type: DNA
A;Residues: 1-542 <KIM>
C;Genetics:
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C:Species: Lactococcus lactis subsp. lactis
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: JN0661
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;Keywords: heat shock; molecular chaperone; stress-induced protein
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             the EMBL Data Library, March 1993
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                                                            06-Jan-1995 #text_change 26-Aug-1999
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AD1333

class I heat-shock protein (chaperonin) GroEL [imported] - Listeria monocytogenes
clspecies: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 *sequence_revision 27-Nov-2001 *text_change 14-Dec-2001
C;Accession: AD133
R;Glaser, P; Frangeul; L.; Buchrieser, C; Amend, A.; Baquero, F; Berche, P.; Bl
C; Dominguez-Bernal, G; Duchaud, E; Durand, L.; Dussurget, O.; Entian, K.D.; Fsi
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J; Kuhn, M; Kunst, F; Kurapkat, G.; Madueno, E.; Maitournam,
A;Authors: Kreft, T; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wr
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD133
A;Status. Tealscines
A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-542 <GLA> A;Residues: 1-542 <GLA> A;Cross-references: GB:NC_003210; PIDN:CAD00146.1; PID:g16411538; GSPDB:GN00177 A;Experimental source: strain EGD-e
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                                                                          A; Status: preliminary
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A;Status: preliminary
A;Molecule type: DNA
A;Residues; 1-542 <BAT's
A;Cross-references: EMBL:X71132; NID:g287869; PIDN:CAA50446.1; PID:g287871
C;Superfamily: chaperonin großL
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cal Similarity 80.4%;
438; Conservative 5
540

    score 2171.5; DB 2; Length
    pred. No. 5.3e-101;
    Mismatches 49; Indels

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class I heat-shock protein (chaperonin) GroEL (imported) - Listeria innocua (strain Clip C;Species: Listeria innocua (crain Clip C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AC1704
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L. M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Madok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1704
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97403.1;
A;Experimental source: strain Clipl1262
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL
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EKLOERLAKLAGGVAVVKVGAATETELKERKLRIEDALNSTRAAVEEGIVAGGGTALVSI
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; Pred. No. 3.96
61; Mismatches
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RESULT 8
548 Holder
541884
58K heat shock protein groEL - Bacillus subtilis
758K heat shock protein groEL - Bacillus subtilis
C; Date: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C; Accession: B41884; B41885; JC1372; B47683; D69637
R; LI, M.; Wong, S.L.
J Bacteriol. 114, 3981-3992, 1992
J Bacteriol. 114, 3981-3992, 1992
A; Title: Cloning and characterization of the groESL operon from Bacillus subtilis.
A; Reference number: A41884; MUID:92283753; PMID:1350776
A; Reference number: A41884; MUID:92283753; PMID:1350776
A; Reference extracted from NCBI backbone (NCBIN:105982, NCBIP:105989)
A; Cross-references: GB:M8132; NID:9143025; PIDN:AAA22503.1; PID:9143027
A; Experimental source: strain 168
A; Reference number: A41885; MUID:92283754; PMID:1350777
A; Reference number: A41885; MUID:92283754; PMID:1350777
A; Reference number: A41885; MUID:92283754; PMID:1350777
A; References: GB:M84965; NID:9143061; PIDN:AAA22531.1; PID:9143063
A; Cross-references: GB:M84965; NID:9143061; PIDN:AAA22531.1; PID:9143063
A; Cross-reference extracted from NCBI backbone (NCBIN:105432, NCBIP:105434)
A; Residues: 1-544 <CSUP.
A; Note: sequence extracted from NCBI backbone (NCBIN:105432, NCBIP:105434)
A; Cross-references: GB:M84965; NID:9143061; PIDN:AAA22531.1; PID:9143063
A; Cross-reference extracted from NCBI backbone (NCBIN:105432, NCBIP:105434)
A; Takahashi, H.; Kawamura, F.; Itaya, M.; Takahashi, H.
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Best Local Similarity
Matches 409; Conserv
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A;Molecule type: protein
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A;Residues: 2-31 <VOL>
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A;Residues: 2-31 A
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A; Cross references: GB:D10972; GB:D01157; NID:94433779; PIDN:BAA22519.1; PII
A; Experimental source: strain Marburg 168
A; Note: the authors translated the codon AAT for residue 15 as Met
R; Volker; U; Mach, H; Schmid, R; Hecker, M.
J. Gen. Microbiol. 138, 2125-2135, 1992
A; Title: Stress proteins and cross-protection by heat shock and salt stress
A; Reference number: A47683; MUID:93123969; PMID:1362210
A; Contents: 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12422.1; PID:g2632916
A;Experimental source: strain 168
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A; Residues: 1-544 <KUN>
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A;Title: Isolation and characterization of the groES and groEL genes
A;Reference number: JC1371; MUID:93129852; PMID:1369494
A;Accession: JC1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Superfamily: chaperonin groBL
;Reywords: heat shock; molecular chaperone; stress-induced protein
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Molecule type: DNA
Residues: 1-14,'N',
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                                                                 EDLGLELKDATMTALGQAAKITVDKDSTVIVEGSGSSEAIANRIALIKSQLETTTSDFDR
                                                                                                                                         QGKPLLLTAEDVEGEALATLVVNKLRGTFNAVAVKAPGFGDRRKAMLEDIAVLTGGEVIT
                                                                                                                                                                            TNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVIT
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B49855
heat shock protein GroEL - Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: (7-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
C;Accession: B49855
R;Schon, U.; Schumann, W.
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A;Title: Molecular cloning, sequencing, and transcriptional analysis of the groESL A;Reference number: A49855; MUID:93224474; PMID:8096841
A;Accession: B49855
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A; Residues: 1-539 <SCH>
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74.98;
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Acta Microbiol. Sin. 36, 241-249, 1996
A:Title: Phylogeny of molecular chaperone 60 proteins.
A:Reference number: JC6063
A:Accession: JC6063
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Residues: 1-544 <XUA>
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Pred. No. 2.5e-93;
4; Mismatches 68;
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heat shock protein TGroEL - thermophilic bacterium PS-3
N;Alternate names: heat shock 61K protein; hsp60
C:Species: thermophilic bacterium PS-3
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Sep-1997
C;Accession: JO1195; pc1252
R;Tanada, H.; Ohta, T.; Hamamoto, T.; Otawara-Hamamoto, Y.; Yanagi, M.; Hiralwa, H.;
Biochem. Biophys. Res. Commun. 179, 565-571, 1991
A;Title: Gene structure of heat shock proteins 61KDa and 12KDa (Thermophilic Chaperor
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C;Superfamily: chaperonin groEL
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: B83720
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A;Experimental source: strain C-125
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A; Residues: 1-544 <STO>
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74; Mismatches
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A;Residues: 1-79 <OHTM
C;Comment: This protein is essential for the formation and restoration of many supramol
C;Superfamily: chaperonin groEL
C;Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: JO1194; MUID:91354309; PMID:1679330
A;Accession: JQ1195
A;Molecule type: DNA
A;Residues: 1-538 GTAM>
A;Residues: 1-538 GTAM>
A;Residues: 1-538 GTAM>
A;Note: Part of this sequence, including both the amino and carboxyl ends of the A;Note: the nucleotide sequence encoding residues 531-538 is not shown in this pa A;Ohta, T:; Honda, K.; Saito, K.; Hayashi, H.; Tano, H.; Hamamoto, T.; Kagawa, Y.
Blochem. Biophys. Res. Commun. 191, 50-557, 1993
A;Title: Heat shock promoter of thermophilic chaperonin operon.
A;Reference number: JC1479; MUID:93213292; PMID:8096382
A;Accession: PC1252
A;A
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  A:Status: preliminary
A:Molecule type: DNA
A;Residues: 1-538 «KUR»
A;Residues: 1-538 «KUR»
A;Cross-references: GB:BA000018; PID:gl3701823; PIDN:BAB43116.1;
A;Experimental source: strain N315
C;GenetLos:
                                                                                                                              GroEL protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 stequence_revision 10-May-2001 stext_change 22-oct-2001
C;Accession: C89994
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L;
Ma, A.; Mizutani-Ui, Y; Kobayashi, N.; Sawano, T; Incue, R; Kaito, C.; Sekimizu,
C.; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticilin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Recession: C89994
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GSPDB:GN00149

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <XUA>
A;Cross-references: DDBJ:D55630; NID:91682949; PIDN:BAA09494.1; PID:91682951
A;Experimental source: strain C-125
C;Genetics:
                                                                             241 QGKPILITAEDVEGEALATLVVNKLRGTFNAVAVKAPGFGDRRKAMLEDIAILTGGEVIT
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                   GEWVDMIKTGIIDPVKVTRSA-LQNAASVASLILTTEAVVANKPEPATPAPAMPAGMDPG 538
GEWYNMVEAGIVDPTKVTRSVPLQHAASV-SAMFTTEAVIADKPEENEGGGGMP--
                                                                                                                                                                 EDLGLELKDATMTALGQAAKITVDKDSTVIVEGSGSSSEAIANRIALIKSQLETTTSDFDR 360
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Pred. No. 1.9e-90;
3; Mismatches 70; Indels 7;
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heat shock protein 60 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 31-Dec-1993 #Sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
C;Accession: JN0601; PN0508
R;Ohta, T.; Honda, K.; Kuroda, M.; Saito, K.; Hayashi, H.
Biochem. Biophys. Res. Commun. 193, 730-737, 1993
A;Title: Molecular characterization of the gene operon of heat shock proteins HSP60 and A;Reference number: JN0600; MUID:93290669; PMID:7916607
A;Accession: JN0601
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JN0601
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A; Residues: 1-539 <0H1>
A; Accession: PN0508
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C; Superfamily: chaperonin groEL
                                                                    Query Match 69.4%; Score 1847.5; DB 2; Length 539; Best Local Similarity 68.3%; Pred. No. 7.1e-85; Matches 371; Conservative 78; Mismatches 87; Indels 7;
                                                                                                                                         Superfamily: chaperonin groEL Reywords: heat shock; stress-induced protein
                                                                                                                                                                                                  Genetics:
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EWVNMLEAGIVDPTKVTRSALQHAASVAAMFLTTEAVVASIPEKNNDQPNM-GGM-PGMM 538
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